

WA



PCT09

#22

RAW SEQUENCE LISTING

DATE: 12/11/2002

PATENT APPLICATION: US/09/869,486B

TIME: 09:28:01

Input Set : N:\Crf4\11192002\I869486A.raw

Output Set: N:\CRF4\12112002\I869486B.raw

1 <110> APPLICANT: Scharenberg, Andrew
 2 <120> TITLE OF INVENTION: CHARACTERIZATION OF THE SOC/CRAC CALCIUM CHANNEL PROTEIN
 FAMILY
 3 <130> FILE REFERENCE: B0662/7026/ERP/KA
 C--> 4 <140> CURRENT APPLICATION NUMBER: US/09/869,486B
 C--> 5 <141> CURRENT FILING DATE: 1998-12-20
 6 <150> PRIOR APPLICATION NUMBER: US 60/114,220
 7 <151> PRIOR FILING DATE: 1998-12-30
 8 <150> PRIOR APPLICATION NUMBER: US 60/120,018
 9 <151> PRIOR FILING DATE: 1999-01-29
 10 <150> PRIOR APPLICATION NUMBER: US 60/140,415
 11 <151> PRIOR FILING DATE: 1999-06-22
 12 <150> PRIOR APPLICATION NUMBER: PCT/US99/29996
 13 <151> PRIOR FILING DATE: 1999-12-20
 14 <160> NUMBER OF SEQ ID NOS: 32
 15 <170> SOFTWARE: PatentIn version 3.0
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 18 <211> LENGTH: 1212
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
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 23 actggaacca aagatcaaga aactgtttgc tctaaagcta cagaaggaga taatacagaa 120
 24 tttggagcat ttgtaggaca cagagatagc atggatttac agaggtttaa agaaacatca 180
 25 aacaagataa aaatactatc caataacaat acttctgaaa acactttgaa acgagtgagt 240
 26 tctcttgctg gatttactga ctgtcacaga acttccattc ctgttcattc aaaacaagaa 300
 27 aaaatcagta gaaggccatc taccgaagac actcatgaag tagattccaa agcagcttta 360
 28 ataccggttt gtagatttca actaaacaga tatatattat taaatacatt aaactttttt 420
 29 agataagatc tacaaagtgg tgatatttgg gactatatca aaaattcaaa aaaatttttc 480
 30 ttaagaaaac tgacttttagc atagtagcag ttacagaaaa gtttcttaca gtgaatagtc 540
 31 aggaatttta aagaaaaatt tatgcagaat aaaggcagga atctcttttt gtttgaattg 600
 32 aagctaatta tatgaactca ttccagcta actgcgataa tgattgattt tgcaaatcc 660
 33 ctttaaaagc acacactgac aagacaaaaa gctcaggaaa aggcaaaaa attactcctt 720
 34 tataatcaag tattatatat aagtcagtgct tcataatttt gctcaagaaa atattgactt 780
 35 acattcatat atatctgttc tggcatagag agattatggt gttaaaaatca tgttattgaa 840
 36 aaaagttatt tcagtgggga aagaggttag ttaacaaaga gattcacagt aacaaatcct 900
 37 cttttctgga gggactcttc ctgaccctga gctgcacaac tttgcaacaa attaaagcct 960
 38 aaccgaagat gacctacaa tggcaattta gaactcatgg gagtcaactt acataaacgg 1020
 39 tatttgattt ctgataagat agtggaaatta ttggttatag atgacaaaat aagtatgttt 1080
 40 aaagtgatga tggacataaa aaagttttta atataaaaca tgagaaaaga aggagatact 1140
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 42 gccgcaagct tt 1212
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 141

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46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
48 <400> SEQUENCE: 2
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52           20           25           30
53   Ala Thr Glu Gly Asp Asn Thr Glu Phe Gly Ala Phe Val Gly His Arg
54     35           40           45
55   Asp Ser Met Asp Leu Gln Arg Phe Lys Glu Thr Ser Asn Lys Ile Lys
56     50           55           60
57   Ile Leu Ser Asn Asn Asn Thr Ser Glu Asn Thr Leu Lys Arg Val Ser
58     65           70           75           80
59   Ser Leu Ala Gly Phe Thr Asp Cys His Arg Thr Ser Ile Pro Val His
60           85           90           95
61   Ser Lys Gln Glu Lys Ile Ser Arg Arg Pro Ser Thr Glu Asp Thr His
62           100          105          110
63   Glu Val Asp Ser Lys Ala Ala Leu Ile Pro Val Cys Arg Phe Gln Leu
64           115          120          125
65   Asn Arg Tyr Ile Leu Leu Asn Thr Leu Asn Phe Phe Arg
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74 <222> LOCATION: (5)..(5)
75 <223> OTHER INFORMATION: a, or c, or g, or t
76 <220> FEATURE:
77 <221> NAME/KEY: Unsure
78 <222> LOCATION: (21)..(22)
79 <223> OTHER INFORMATION: a, or c, or g, or t
80 <220> FEATURE:
81 <221> NAME/KEY: Unsure
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83 <223> OTHER INFORMATION: a, or c, or g, or t
84 <400> SEQUENCE: 3

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86   aattgatgtg tgtgcaaacg attctgttat cctcaaatc tgtggtcctg ggacgtgggt      120
87   gactccattt cttcaagcag tctacctctt tgwacagtat atcattatgg ttaatcttct      180
88   tattgcattt ytcaacaatg tgtattttaca agtgaaggca atttccaata ttgyatggaa      240
89   gtaccagcgt tatcatttta ttatggctta tcatgagaaa ccagttctgc ctctccact      300
90   tatcattctt agccatatag tttctctgtt ttgctgcata tgtaagagaa gaaagaaaga      360
91   taagacttcc gatggaccaa aacttttctt aacagaagaa gatcaaaaaga aacttcatga      420
92   ttttgaagag cagtgtgttg aaatgtattt caatgaaaaa gatgacaaat ttcattctgg      480
93   gagtgaagag agaattcgtg tcacttttga aagagtggaa cagatgtgca ttcagattaa      540
94   agaagttgga gatccgtgtc aactacataa aaagatcatt acaatcatta gattctcaaa      600
95   ttggccattt gcaagatctt tcagccctga cggtagatac attaaaaaca ctactggcc      660

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96      aaaagcgtcg gaagctagca aagttcataa tgaaatcaca cgagaactga gcattttcaa      720
97      acacttggtc caaaacctt                                     739
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100 <211> LENGTH: 235
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102 <213> ORGANISM: Homo sapiens
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105 <222> LOCATION: (41)..(41)
106 <223> OTHER INFORMATION: any amino acid
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109 <222> LOCATION: (54)..(54)
110 <223> OTHER INFORMATION: any amino acid
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113 <222> LOCATION: (69)..(69)
114 <223> OTHER INFORMATION: any amino acid
115 <400> SEQUENCE: 4
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118      Asp Ser Val Ile Pro Gln Ile Cys Gly Pro Gly Thr Trp Leu Thr Pro
119      20              25              30
W--> 120      Phe Leu Gln Ala Val Tyr Leu Phe Xaa Gln Tyr Ile Ile Met Val Asn
121      35              40              45
W--> 122      Leu Leu Ile Ala Phe Xaa Asn Val Tyr Leu Gln Val Lys Ala Ile
123      50              55              60
W--> 124      Ser Asn Ile Trp Xaa Lys Tyr Gln Arg Tyr His Phe Ile Met Ala Tyr
125      65              70              75              80
126      His Glu Lys Pro Val Leu Pro Pro Pro Leu Ile Ile Leu Ser His Ile
127      85              90              95
128      Val Ser Leu Phe Cys Cys Ile Cys Lys Arg Arg Lys Lys Asp Lys Thr
129      100             105             110
130      Ser Asp Gly Pro Lys Leu Phe Leu Thr Glu Glu Asp Gln Lys Lys Leu
131      115             120             125
132      His Asp Phe Glu Glu Gln Cys Val Glu Met Tyr Phe Asn Glu Lys Asp
133      130             135             140
134      Asp Lys Phe His Ser Gly Ser Glu Glu Arg Ile Arg Val Thr Phe Glu
135      145             150             155             160
136      Arg Val Glu Gln Met Cys Ile Gln Ile Lys Glu Val Gly Asp Pro Cys
137      165             170             175
138      Gln Leu His Lys Lys Ile Ile Thr Ile Ile Arg Phe Ser Asn Trp Pro
139      180             185             190
140      Phe Ala Arg Ser Phe Ser Pro Asp Gly Arg Tyr Ile Lys Asn Thr His
141      195             200             205
142      Trp Pro Lys Ala Ser Glu Ala Ser Lys Val His Asn Glu Ile Thr Arg
143      210             215             220
144      Glu Leu Ser Ile Ser Lys His Leu Ala Gln Asn
145      225             230             235

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Input Set : N:\Cr4\11192002\I869486A.raw

Output Set: N:\CRF4\12112002\I869486B.raw

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156 <221> NAME/KEY: Unsure
157 <222> LOCATION: (482)..(482)
158 <223> OTHER INFORMATION: a, or c, or g, or t
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162      ttgtaatat ttaatgaaag atgacaaaaga tccccagtggt aatatatttg gtcaagactt      180
163      acctgcagta ccccagagaa aagaatttaa ttttccagag gctggttcct cttctggtgc      240
164      cttattccca agtgctgttt cccctccaga actgcgacag agactacatg gggtagaact      300
165      cttaaaaata tttaataaaa atcaaaaatt aggcagttca tctactagca taccacatct      360
W--> 166      gtcattccsca csarscaaat tttttgntag tacaccatct cagccaagtt gcaaaaagcca      420
167      cttggaaact ggaaccaaag atcaagaaac tgtttgctct aaagctacag aaggagataa      480
W--> 168      tncagaattt ggagcatttg taggacacag agatagcatg gatttacaga ggttttaaga      540
169      aacatcaaac aagataaaaa tactatccaa taacaatact tctgaaaaaca ctttgaaacg      600
170      agtgagttct cttgctggat ttactgactg tcacagaact tccattcctg ttcatcctaa      660
171      acaagaaaaa atcagtagaa ggccatctac cgaagacact catgaagtag attccaaagc      720
172      agctttaata ccggtttgta gatttcaact aaacagatat atattattaa atacattaaa      780
173      cttttttaga taagatctac aaagtgggta tatttgggac tatatcaaaa attcaaaaaa      840
174      atttttctta agaaaactga ctttagcata gtagcagtta cagaaaagtt tcttacagtg      900
175      aatagtcagg aatttttaaag aaaaatttat gcagaataaa ggcaggaatc tctttttgtt      960
176      tgaattgaag ctaattatat gaactcattt ccagctaact gcgataatga ttgattttgc      1020
177      aaattccctt taaaagcaca cactgacaag acaaaaagct caggaaaagg cagaaaaatt      1080
178      actcctttat aatcaagtat tatatataag tcagtgtctc taattttgct caagaaaata      1140
179      ttgacttaca ttcatatata tctgttctgg catagagaga ttatgttggt aaaatcatgt      1200
180      tattgaaaaa agttatttca gtggggaaag aggttagtta acaaagagat tcacagtaac      1260
181      aaatcctcct ttctggaggg actcttcctg accctgagct gcacaacttt gcaacaaatt      1320
182      aaagcctaac cgaagatgac ctcaaatgg caatttagaa ctcatgggag tcaacttaca      1380
183      taaacggtat ttgatttctg ataagatagt ggaattattg gttatagatg acaaaaataag      1440
184      tatgtttaaa gtgatgatgg acataaaaaa gttttaaata taaaacatga gaaaagaagg      1500
185      agatactatt caaaaagact ggcaaatattg aaaaactaga aataaaaaaa aaaaaaaaaa      1560
186      atgagcggcc gcaagcttt      1579
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191 <213> ORGANISM: Homo sapiens
192 <220> FEATURE:
193 <221> NAME/KEY: UNSURE
194 <222> LOCATION: (103)..(105)
195 <223> OTHER INFORMATION: any amino acid
196 <220> FEATURE:

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Output Set: N:\CRF4\12112002\I869486B.raw

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197 <221> NAME/KEY: UNSURE
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199 <223> OTHER INFORMATION: any amino acid
200 <220> FEATURE:
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202 <222> LOCATION: (141)..(141)
203 <223> OTHER INFORMATION: any amino acid
204 <400> SEQUENCE: 6
205 Val Asn Thr Leu Ser Ser Ser Leu Pro Gln Gly Asp Leu Glu Ser Asn
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207 Asn Pro Phe His Cys Asn Ile Leu Met Lys Asp Asp Lys Asp Pro Gln
208 20 25 30
209 Cys Asn Ile Phe Gly Gln Asp Leu Pro Ala Val Pro Gln Arg Lys Glu
210 35 40 45
211 Phe Asn Phe Pro Glu Ala Gly Ser Ser Ser Gly Ala Leu Phe Pro Ser
212 50 55 60
213 Ala Val Ser Pro Pro Glu Leu Arg Gln Arg Leu His Gly Val Glu Leu
214 65 70 75 80
215 Leu Lys Ile Phe Asn Lys Asn Gln Lys Leu Gly Ser Ser Ser Thr Ser
216 85 90 95
W--> 217 Ile Pro His Leu Ser Ser Xaa Xaa Xaa Lys Phe Phe Xaa Ser Thr Pro
218 100 105 110
219 Ser Gln Pro Ser Cys Lys Ser His Leu Glu Thr Gly Thr Lys Asp Gln
220 115 120 125
W--> 221 Glu Thr Val Cys Ser Lys Ala Thr Glu Gly Asp Asn Xaa Glu Phe Gly
222 130 135 140
223 Ala Phe Val Gly His Arg Asp Ser Met Asp Leu Gln Arg Phe Lys Glu
224 145 150 155 160
225 Thr Ser Asn Lys Ile Lys Ile Leu Ser Asn Asn Asn Thr Ser Glu Asn
226 165 170 175
227 Thr Leu Lys Arg Val Ser Ser Leu Ala Gly Phe Thr Asp Cys His Arg
228 180 185 190
229 Thr Ser Ile Pro Val His Ser Lys Gln Glu Lys Ile Ser Arg Arg Pro
230 195 200 205
231 Ser Thr Glu Asp Thr His Glu Val Asp Ser Lys Ala Ala Leu Ile Pro
232 210 215 220
233 Val Cys Arg Phe Gln Leu Asn Arg Tyr Ile Leu Leu Asn Thr Leu Asn
234 225 230 235 240
235 Phe Phe Arg
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238 <211> LENGTH: 3532
239 <212> TYPE: DNA
240 <213> ORGANISM: Mus musculus
241 <220> FEATURE:
242 <221> NAME/KEY: Unsure
243 <222> LOCATION: (2420)..(2420)
244 <223> OTHER INFORMATION: a, or c, or g, or t
245 <220> FEATURE:
246 <221> NAME/KEY: Unsure

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/11/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 5,21,22,29
Seq#:4; Xaa Pos. 41,54,69
Seq#:5; N Pos. 387,482
Seq#:6; Xaa Pos. 103,104,105,109,141
Seq#:7; N Pos. 2420,2434,2461,2466,2470
Seq#:9; N Pos. 5094
Seq#:18; N Pos. 6,58,89,406
Seq#:19; Xaa Pos. 15,25,131
Seq#:23; N Pos. 2382,4664,4682,4702,5038,5039,5056,5071,5072
Seq#:24; Xaa Pos. 794
Seq#:26; Xaa Pos. 553,603
Seq#:27; N Pos. 158,6966,6984,7004,7340,7341,7358,7373,7374

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2